

Figure 1A

1 ATGACAACCTCTTGTTCCTGCAACCCCTCTCCTTCTTCTCTCTGGACCCCTGCCAGGGCAG 60
 1 M T T L V P A T L S F L L L W T L P G Q 20

 61 GTCCTCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG 120
 21 V L L R V A L A K E E V K S G T K G S Q 40

 121 CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGCGAACATCTGGATATGATGCC 180
 41 P M S P S D F L D K L M G R T S G Y D A 60

 181 AGGATTCGGCCCAATTTTAAAGGCCCAACCGTGAACGTGACCTGCAACATCTTCATCAAC 240
 61 R I R P N F K G P P V N V T C N I F I N 80

 241 AGTTTCAGCTCCGTACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGGCGCAA 300
 81 S F S S V T K T T M D Y R V N V F L R Q 100

 301 CAGTGAATGACCCACGCGCTGTCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT 360
 101 Q W N D P R L S Y R E Y P D D S L D L D 120

 361 CCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGTCTAATGAGAAAGGGGCC 420
 121 P S M L D S I W K P D L F F A N E K G A 140

 421 AACTTCCATGAGGTGACCAAGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG 480
 141 N F H E V T T D N K L L R I F K N G N V 160

 481 CTGTACAGCATCAGGTGACCCCTCATTTTGTCTGCCTGATGGACCTCAAGAACTTCCCC 540
 161 L Y S I R L T L I L S C L M D L K N F P 180

 541 ATGGACATCCAGACCTGCACGATGCAGCTTGAGAGCTTTGGCTACACCATGAAAGACCTC 600
 181 M D I Q T C T M Q L E S XXXXXXXXXX T M K D L 200

 601 GTGTTTGAGTGGCTGGAAGATGCTCCTGCTGCCAAGTGGCTGAGGGGCTGACTCTGCC 660
 201 V F E W L E D A P A V Q V A E G L T L P 220

 661 CAGTTTATCTTCCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGG 720
 221 Q F I L R D E K D L G C C T XXXXXXXXXX G 240

 721 AAATTACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT 780
 241 K F T C I E V K F H L E R Q M G Y Y L I 260

 781 CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCTCCTTCTCGGATCAAC 840
 261 Q M Y I P S L L I V I L S W V S F W I N 280

 841 ATGGATGCTGCCCTGCCCCGTGTGGGCTGGGCATCACCAACGCTGTACCATGACCACC 900
 281 M D A A P A R V G L G I T T V L T M T T 300

100% GC content
 100% GC content

Figure 1B

901	CAGAGCTCTGGCTCCCGGGCTCTTTGCCTAAGGTGCTCTACGTGAAGGCAATCGACATC	960
301	<u>Q S S G S</u> R A S L P K V S Y V K A I D I	320
961	TGGATGGCTGTGTGCTGCTCTTTGTGTTGCTGCTTGCTGGAGTATGCTGCCATAAAT	1020
321	<u>W M A V C L L F V F A A L L E Y A A I N</u>	340
1021	TTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGGCCCAACGC	1080
341	<u>F V S</u> R Q H K E F I R L R R R Q R R Q R	360
1081	TTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCTGGCTATGGCTTGGGCCAC	1140
361	L E E D I I Q E S R F Y F R G Y G L G H	380
1141	TGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCT	1200
381	C L Q A R D G G P M E G S G I Y S P Q P	400
1201	CCAGCCCCCTCTTCTAAGGGAAGGAGAAACCACGCGAAACTCTACGTGGACTGAGCCAAG	1260
401	P A P L L R E G E T T R K L Y V D	417
1261	AGAATTGACACCATCTCCCGGGCTGCTTCCCTTTCACCTTCCTCATCTTCAATATCTTC	1320
1321	TACTGGGTGTCTATAAAGTGCTACGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGG	1380
1381	TGGGAGCTATAGAGTCTCTGCTGCTGGCCTCCTGCTTCCTCTGCTGGGTGGGCTTCTCCCTC	1440
1441	AGTTAGACTCCATTAGGGGTTTGGACAGTTCCCTTCCTGATCTCCCACTCAGAACTTCAAC	1500
1501	TACCAGTCCCAAAGCTATGTGGGCCTATATTGCGATGGTGCCAATGGTGGCTGTACTTATA	1560
1561	AAGATGGCTTATCTACCCTAGTCCATATTTTCTCCATACTTTCCCAATTCTCATGAGACT	1620
1621	AAGGTTTGGCCACATCTCCTGGGGCCAGGATGACCTTCTGCCCCCTGCTGGAGCCCTCCCTGT	1680
1681	TTTCCAATACTCCAGTGGAGAGTATTGAGAACACTGCTGCTAGATTCTGGCATTGTGCAT	1740
1741	CTTAATCTGCACCACTTCTCCCCCTGCCACCTCCCACCCAGAGCCTGGCCATTACTCTGT	1800
1801	CCTCTGTCCCTCCTGCTGCAGATTCAATGGTGAGTTTCTCCTATCCACAAGTGTGCCCC	1860
1861	TGTGGGGCCTAGTCAGGTTTCTTGAAGTGAGAGGAAGGCAAGCCGCAAGTTCCCCACC	1920
1921	TCTCGAGAGGGTTGGAACAGTCATAGGCTGCACTGGGCTAGCGACTATATGGCCCCAACAG	1980

CCAGCCCCCTCTTCTAAGGGAAGGAGAAACCACGCGAAACTCTACGTGGACTGAGCCAAG

Figure 1C

1981 AGAGGTGTTCAAGTCTCTTGGGAAGCCCCACACTTTGTCTTCATCCCTTTTCTATTGCG 2040
 2041 CTTGTCTGCTCTTTCTGTTCAGTCTGAGATACTCCTCTTGTCTGTCTCTTAGITTTGAGGA 2100
 2101 GAGCGTTCTGAGCTGACCAGGGTAGCTGGTTCAGAAATTACTGTGAGAATTGGGGCAGAG 2160
 2161 ACTTTGGGTTCTCAAAAAGACTAACCTTCCAGATCCACCTGAACATTCTGGTCTCAGAAA 2220
 2221 TATTCGTTCCGTTCCCTAATTAAGTACATGGTGGCAGGATCTGTTGGACAGCTGGGGAG 2280
 2281 TGTAAAAAAGAAAAATACTTGTCTTTAAGAAACTTACTTTATGATGCTAGAAAACCTT 2340
 2341 TGAGAAAAGTGAGATCCAAGGTAGTGAACCCAGGAGGAGTAGAATAGAGAACTATTCT 2400
 2401 CAGAGTGTCTTTTGTGGCTGGGCTTTCATTTGTTTCTCTTTCTCACCAAAGCTATTT 2460
 2461 TCCAGGGCCCTTCATTTCCAACCTGGTCTTTCACCTCCTTTTGGTGTGCAATAAAGGTG 2520
 2521 CCGCTGCAACCTTGTTAAGGATAAAAAAAAAAAAAAAAAAAAAA 2565

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Figure 2A

1	ATGACAACCTCTTGTTCCTGCAACCCCTCTCCTTCTTCTCTGGAACCTGCCAGGGCAG	60
1	M T T L V P A T L S F L L L W T L P G Q	20
61	GTCCTCCTCAGGGTGGCCTTGGCAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCAG	120
21	V L L R V A L A K E E V K S G T K G S Q	40
121	CCCATGTCCCCCTCTGATTTCTTAGACAAACTTATGGGCGAACATCTGGATATGATGCC	180
41	P M S P S D F L D K L M G R T S G Y D A	60
181	AGGATTTCGGCCCAATTTTAAAGGCCCAACCGTGAACGTGACCTGCAACATCTTCATCAAC	240
61	R I R P N F K G P P V N V T C N I F I N	80
241	AGTTTCAGCTCCGTACCAAGAACCAATGGACTACCGGGTGAATGTCTTCTTCCGGCAA	300
81	S F S S V T K T T M D Y R V N V F L R Q	100
301	CAGTGGAAATGACCCACGCGCTGTCTACGAGAATATCCTGATGACTCTCTGGAACCTCGAT	360
101	Q W N D P R L S Y R E Y P D D S L D L D	120
361	CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGTCTAATGAGAAAGGGGCC	420
121	P S M L D S I W K P D L F F A N E K G A	140
421	AACTTCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG	480
141	N F H E V T T D N K L L R I F K N G N V	160
481	CTGTACAGCATCAGGCTGACCCCTCATTTTGTCTGCGTATGGAACCTCAAGAATCTCCCC	540
161	L Y S I R L T L I L S C L M D L K N F P	180
541	ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG	600
181	M D I Q T C T M Q L E S S S I L C S P L	200
601	CCATCTCTGTCACTTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTGAGTGGCTGGAA	660
201	P S L S L S V XXXXXXXXXX T M K D L V F E W L E	220
661	GATGCTCCTGTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGGCGGAT	720
221	D A P A V Q V A E G L T L P Q F I L R D	240
721	GAGAAGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCGAG	780
241	E K D L G C C T XXXXXXXXXX G K F T C I E	260
781	GTAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTGAGATGACATCCCCAGC	840
261	V K F H L E R Q <u>M G Y Y L I Q M Y I P S</u>	280
841	CTACTCATCGTCATCCTGTCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCTGCC	900
281	<u>L L I V I L S W V S F W I N M</u> D A A P A	300

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Figure 2B

901 CGTGTGGGCTGGGCATCACCAACCGTCTCACCATGACCACCCAGAGCTCTGGCTCCCGG 960
 301 R V G L G I T T V L T M T T Q S S G S R 320

 961 GCCTCTTTGCCTAAGGTGTCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTCTG 1020
 321 A S L P K V S Y V K A I D I W M A V C L 340

 1021 CTCTTTGTGTCTGCTGCCTTGTCTGGAGTATGCTGCCATAAATTTTGTTCCTGTCAGCAT 1080
 341 L F V F A A L L E Y A A I N F V S R Q H 360

 1081 AAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATC 1140
 361 K E F I R L R R R Q R R Q R L E E D I I 380

 1141 CAAGAAAGTCGTTTCTATTTCCTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT 1200
 381 Q E S R F Y F R G Y G L G H C L Q A R D 400

 1201 GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCAACCTCCAGCCCTCTTCTAAGG 1260
 401 G G P M E G S G I Y S P Q P P A P L L R 420

 1261 GAAGGAGAAACCAACGCGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC 1320
 421 E G E T T R K L Y V D 431

 1321 CGGGCTGTCTTCCCTTTCTACTTTCCTCATCTTCAATATCTTCTACTGGGTGTCTATAAA 1380

 1381 GTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCCT 1440

 1441 GCTGCTGGCTCCTGCTTCTCCTCTGGGTGGGCTTTCTCCCTCAGTTAGACTCCATTAGGG 1500

 1501 GTTTGGACAGTTCCTTCTCTGATCTCCCACTCAGAAGTCAACTACCAAGTCCCAAAGCTAT 1560

 1561 GTGGGCCTATATGTCATGGTGCCAAATGGTGGCTGTACTTATAAAGATGGCTTATCTACCC 1620

 1621 TAAAAAAAAAAAAAAAAAAAA 1640

10075046:21700
 20075046:21700

Figure 3A

1 50

GRA1_HUMAN (1) -----MYSFNTLRILSLGSAVFSLAAEKALVARSATPMSPSDFLDK
 GRA3_HUMAN (1) -MAHVRHFRRLVSGCTDEAALLLSLWAKETLSKRSAPMSPSDFLDK
 HGRA4 (1) MTTLPATLSELLLTLPGLVLLRALAKEEVKSGTKGSQPMSPSDFLDK
 HGRA4sv (1) MTTLPVATSELLLTLPGLVLLRALAKEEVKSGTKGSQPMSPSDFLDK
 GRA4_MOUSE (1) -----VALAKEEVKSGTKGSQPMSPSDFLDK
 GRA2_HUMAN (1) MNROIVNIIALAHLELTNHRTEFCKDILSRSGCKPSQMSPSDFLDK

51 100

GRA1_HUMAN (45) LMGRTSGYDARLPNFKGPPVNVNCNIFINSGSVTETMDYRVNFIHQ
 GRA3_HUMAN (50) LMGRTSGYDARLPNFKGPPVNVNCNIFINSGSVTETMDYRVNFIHQ
 HGRA4 (51) LMGRTSGYDARLPNFKGPPVNVNCNIFINSGSVTETMDYRVNFIHQ
 HGRA4sv (51) LMGRTSGYDARLPNFKGPPVNVNCNIFINSGSVTETMDYRVNFIHQ
 GRA4_MOUSE (27) LMGRTSGYDARLPNFKGPPVNVNCNIFINSGSVTETMDYRVNFIHQ
 GRA2_HUMAN (51) LMGRTSGYDARLPNFKGPPVNVNCNIFINSGSVTETMDYRVNFIHQ

101 150

GRA1_HUMAN (95) QNDRRLVSEYPPDSDLDPMSLDLSIWKPDLFANKEGANFHEVITDNK
 GRA3_HUMAN (100) QNDRRLVSEYPPDSDLDPMSLDLSIWKPDLFANKEGANFHEVITDNK
 HGRA4 (101) QNDRRLVSEYPPDSDLDPMSLDLSIWKPDLFANKEGANFHEVITDNK
 HGRA4sv (101) QNDRRLVSEYPPDSDLDPMSLDLSIWKPDLFANKEGANFHEVITDNK
 GRA4_MOUSE (77) QNDRRLVSEYPPDSDLDPMSLDLSIWKPDLFANKEGANFHEVITDNK
 GRA2_HUMAN (101) QNDRRLVSEYPPDSDLDPMSLDLSIWKPDLFANKEGANFHEVITDNK

151 200

GRA1_HUMAN (145) LLRISSKNGNVLYSIRLTITLISCPMDLKNPFMDIQTCIVQLES
 GRA3_HUMAN (150) LLRIFFKNGNVLYSIRLTITLISCPMDLKNPFMDIQTCIVQLES
 HGRA4 (151) LLRIFFKNGNVLYSIRLTITLISCPMDLKNPFMDIQTCIVQLES
 HGRA4sv (151) LLRIFFKNGNVLYSIRLTITLISCPMDLKNPFMDIQTCIVQLES
 GRA4_MOUSE (127) LLRIFFKNGNVLYSIRLTITLISCPMDLKNPFMDIQTCIVQLES
 GRA2_HUMAN (151) LLRISSKNGNVLYSIRLTITLISCPMDLKNPFMDIQTCIVQLES

201 250

GRA1_HUMAN (187) -----FGYIMNDLIFEWQELGAVQVVEGLTLPGFLLPEKIDRYQYCKH
 GRA3_HUMAN (192) -----FGYIMNDLIFEWQELGAVQVVEGLTLPGFLLPEKIDRYQYCKH
 HGRA4 (193) -----FGYIMNDLIFEWQELGAVQVVEGLTLPGFLLPEKIDRYQYCKH
 HGRA4sv (201) PSLSLSVGYTMDIFEWQELGAVQVVEGLTLPGFLLPEKIDRYQYCKH
 GRA4_MOUSE (169) -----FGYIMNDLIFEWQELGAVQVVEGLTLPGFLLPEKIDRYQYCKH
 GRA2_HUMAN (193) -----FGYIMNDLIFEWQELGAVQVVEGLTLPGFLLPEKIDRYQYCKH

251 300

GRA1_HUMAN (230) [<-----<TM1>----->] YNTGKFTCTIEVFHLERQMGGYLIQMYIPSLILVILSWSFWINMDAAP
 GRA3_HUMAN (235) YNTGKFTCTIEVFHLERQMGGYLIQMYIPSLILVILSWSFWINMDAAP
 HGRA4 (237) YNTGKFTCTIEVFHLERQMGGYLIQMYIPSLILVILSWSFWINMDAAP
 HGRA4sv (251) YNTGKFTCTIEVFHLERQMGGYLIQMYIPSLILVILSWSFWINMDAAP
 GRA4_MOUSE (213) YNTGKFTCTIEVFHLERQMGGYLIQMYIPSLILVILSWSFWINMDAAP
 GRA2_HUMAN (236) YNTGKFTCTIEVFHLERQMGGYLIQMYIPSLILVILSWSFWINMDAAP

3[<-----<TM2>----->] [<-----<TM3>----->]

GRA1_HUMAN (280) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMWAVCLLFVSLLEY
 GRA3_HUMAN (285) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMWAVCLLFVSLLEY
 HGRA4 (287) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMWAVCLLFVSLLEY
 HGRA4sv (301) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMWAVCLLFVSLLEY
 GRA4_MOUSE (263) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMWAVCLLFVSLLEY
 GRA2_HUMAN (286) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMWAVCLLFVSLLEY

Figure 3B

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>>>>>>]
GRA1_HUMAN (330) AAVNFYSRCHKEFLRRLRRRR-----HHEDEAGELRNFNS 400
GRA3_HUMAN (335) AAVNFYSRCHKEFLRRLRRRRRNKTEAFLEKFYRFSDMDEVRERFSF
HGRA4 (337) AAVNFYSRCHKEFLRRLRRRR-----RQRLEEDTQESRFYFR
HGRA4sv (351) AAVNFYSRCHKEFLRRLRRRR-----RQRLEEDTQESRFYFR
GRA4_MOUSE (313) AAVNFYSRCHKEFLRRLRRRR-----RQRLEEDTQESRFYFR
GRA2_HUMAN (336) AAVNFYSRCHKEFLRRLRRRR-----RQRLEEDTQESRFYFR

401
GRA1_HUMAN (366) YGGMGPACLQAKDGISVKGANSGNTNPPPPAPSRPEEMRKLFQRAKKI 450
GRA3_HUMAN (385) YGGMGP-CLQAKDGMTPKGDN-----HPVQVHPKQPEMRKLFQRAKKI
HGRA4 (375) YGGLGH-CLQARDGGPMHGS-CIYSQPPAPLLEGETTRKLFVD----
HGRA4sv (389) YGGLGH-CLQARDGGPMHGS-CIYSQPPAPLLEGETTRKLFVD----
GRA4_MOUSE (338) -----
GRA2_HUMAN (374) YGGMGH-CLQAKDGTAKKTPANPLQPPK----EGDAKKKFVDRAKKI

451
GRA1_HUMAN (416) DKISRIGFPAFLIFNPFYWITYKIRREDTHNQ--- 487
GRA3_HUMAN (429) DTISRACFPAFLIFNPFYWITYKIRHEDTHHQQQD
HGRA4 (418) -----
HGRA4sv (432) -----
GRA4_MOUSE (338) -----
GRA2_HUMAN (419) DTISRAAFPAFLIFNPFYWITYKIRHEDTHHK---

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10079 NP

Figure 4

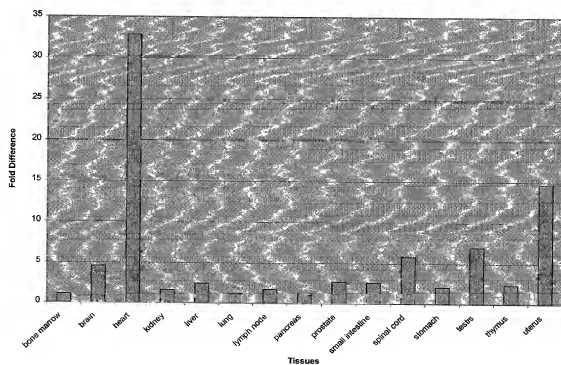


Figure 5

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G1934909_001 MTLVLPATLSFLLWTLPGQVLLRVALAKEEVKSGTKSQPMSPSDFLDKLMGRTSGYDA
cloneE3      MTLVLPATLSFLLWTLPGQVLLRVALAKEEVKSGTKSQPMSPSDFLDKLMGRTSGYDA
cloneD8      MTLVLPATLSFLLWTLPGQVLLRVALAKEEVKSGTKSQPMSPSDFLDKLMGRTSGYDA
*****

G1934909_001 RIRPNFKGPPVNVTCNIFINSFSSITKTTMACWAPGNGNVSEGPISAPSQYRVNVFLRQ
cloneE3      RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ
cloneD8      RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ
*****
: : .: .:*****

G1934909_001 QWNPRLSYREYPDDSLDLPMSLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV
cloneE3      QWNPRLSYREYPDDSLDLPMSLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV
cloneD8      QWNPRLSYREYPDDSLDLPMSLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV
*****

G1934909_001 LYSIRLTLILSCLMDLKNFPMDIQTCTMOLES-----FGYTMKDLVFEWLE
cloneE3      LYSIRLTLILSCLMDLKNFPMDIQTCTMOLES-----FGYTMKDLVFEWLE
cloneD8      LYSIRLTLILSCLMDLKNFPMDIQTCTMOLES-----FGYTMKDLVFEWLE
*****

G1934909_001 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPS
cloneE3      DAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPS
cloneD8      DAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPS
*****

G1934909_001 LLIVILSWVSFWINMDAAPARVGLGITTVLMTTQSSGSRASLPK-----
cloneE3      LLIVILSWVSFWINMDAAPARVGLGITTVLMTTQSSGSRASLPKVSYPKADINMAVCL
cloneD8      LLIVILSWVSFWINMDAAPARVGLGITTVLMTTQSSGSRASLPKVSYPKADINMAVCL
*****

G1934909_001 -----
cloneE3      LFVFAALLEYAAINFVSRQHKEFIRLRERQRRQRLIEDIIQESFYFRGYGLGHCLQARD
cloneD8      LFVFAALLEYAAINFVSRQHKEFIRLRERQRRQRLIEDIIQESFYFRGYGLGHCLQARD

G1934909_001 -----
cloneE3      GGPMEGSGIYSPQPAPLLREGETTRKLYVD
cloneD8      GGPMEGSGIYSPQPAPLLREGETTRKLYVD

```

Figure 6.

HGRA4

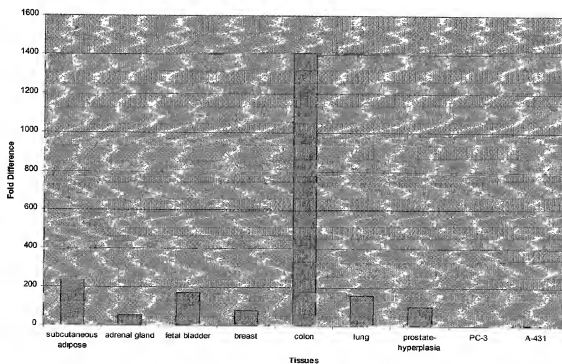
<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.8%	82.2%
human glycine receptor alpha 3 subunit	gi 5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi 817957	97%	96%
human glycine receptor alpha 2 subunit	gi 4504021	80.6%	86.5%

HGRA4sv

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi 5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi 817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi 4504021	80.3%	86.2%

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Figure 8



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